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## RAW SEQUENCE LISTING

DATE: 10/31/2001

PATENT APPLICATION: US/09/938,497

TIME: 12:04:25

Input Set : N:\Crf3\RULE60\09938497.txt

Output Set: N:\CRF3\10312001\I938497.raw

## SEQUENCE LISTING

## 3 (1) GENERAL INFORMATION:

5 (i) APPLICANT: WASTFALT, Maria K. Boden

6 FLOCK, Jan-Ingmar

8 (ii) TITLE OF INVENTION: FIBRINOGEN BINDING PROTEIN

10 (iii) NUMBER OF SEQUENCES: 15

12 (iv) CORRESPONDENCE ADDRESS:

13 (A) ADDRESSEE: BURNS, DOANE, SWECKER &amp; MATHIS

14 (B) STREET: P.O. Box 1404

15 (C) CITY: Alexandria

16 (D) STATE: Virginia

17 (E) COUNTRY: United States

18 (F) ZIP: 22313-1404

20 (v) COMPUTER READABLE FORM:

21 (A) MEDIUM TYPE: Floppy disk

22 (B) COMPUTER: IBM PC compatible

23 (C) OPERATING SYSTEM: PC-DOS/MS-DOS

24 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

26 (vi) CURRENT APPLICATION DATA:

C--&gt; 27 (A) APPLICATION NUMBER: US/09/938,497

C--&gt; 28 (B) FILING DATE: 27-Aug-2001

29 (C) CLASSIFICATION:

39 (vii) PRIOR APPLICATION DATA:

32 (A) APPLICATION NUMBER: 09/276,141

33 (B) FILING DATE:

36 (A) APPLICATION NUMBER: SE 9302955-1

37 (B) FILING DATE: 13-SEP-1993

40 (A) APPLICATION NUMBER: WO PCT/SE93/00759

41 (B) FILING DATE: 20-SEP-1993

43 (viii) ATTORNEY/AGENT INFORMATION:

44 (A) NAME: McGowan, Malcolm K.

45 (B) REGISTRATION NUMBER: 39,300

46 (C) REFERENCE/DOCKET NUMBER: 012889-011

48 (ix) TELECOMMUNICATION INFORMATION:

49 (A) TELEPHONE: (703) 836-6620

50 (B) TELEFAX: (703) 836-2021

53 (2) INFORMATION FOR SEQ ID NO: 1:

55 (i) SEQUENCE CHARACTERISTICS:

56 (A) LENGTH: 20 amino acids

57 (B) TYPE: amino acid

58 (C) STRANDEDNESS: single

59 (D) TOPOLOGY: linear

61 (ii) MOLECULE TYPE: protein

63 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

65 Ile Val Thr Lys Asp Tyr Ser Lys Glu Ser Arg Val Asn Glu Asn Ser

66 1 5 10 15

68 Lys Tyr Gly Thr

ENTERED

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69                20
72 (2) INFORMATION FOR SEQ ID NO: 2:
74     (i) SEQUENCE CHARACTERISTICS:
75         (A) LENGTH: 20 amino acids
76         (B) TYPE: amino acid
77         (C) STRANDEDNESS: single
78         (D) TOPOLOGY: linear
80     (ii) MOLECULE TYPE: protein
82     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
84     Ile Val Thr Lys Asp Tyr Ser Lys Glu Ser Arg Val Asn Glu Lys Ser
85     1             5             10             15
87     Lys Lys Gly Ala
88                20
91 (2) INFORMATION FOR SEQ ID NO: 3:
93     (i) SEQUENCE CHARACTERISTICS:
94         (A) LENGTH: 20 amino acids
95         (B) TYPE: amino acid
96         (C) STRANDEDNESS: single
97         (D) TOPOLOGY: linear
99     (ii) MOLECULE TYPE: protein
101    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
103    Ile Val Thr Lys Asp Tyr Ser Gly Lys Ser Gln Val Asn Ala Gly Ser
104    1             5             10             15
106    Lys Asn Gly Thr
107                20
110 (2) INFORMATION FOR SEQ ID NO: 4:
112    (i) SEQUENCE CHARACTERISTICS:
113        (A) LENGTH: 20 amino acids
114        (B) TYPE: amino acid
115        (C) STRANDEDNESS: single
116        (D) TOPOLOGY: linear
118    (ii) MOLECULE TYPE: protein
120    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
122    Ile Val Thr Lys Asp Tyr Ser Gly Lys Ser Gln Val Asn Ala Gly Ser
123    1             5             10             15
125    Lys Asn Gly Thr
126                20
129 (2) INFORMATION FOR SEQ ID NO: 5:
131    (i) SEQUENCE CHARACTERISTICS:
132        (A) LENGTH: 20 amino acids
133        (B) TYPE: amino acid
134        (C) STRANDEDNESS: single
135        (D) TOPOLOGY: linear
137    (ii) MOLECULE TYPE: protein
139    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
141    Ser Glu Gly Tyr Gly Pro Arg Glu Lys Lys Pro Val Ser Ile Asn His
142    1             5             10             15
144    Asn Ile Val Glu
145                20

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## 148 (2) INFORMATION FOR SEQ ID NO: 6:

## 150 (i) SEQUENCE CHARACTERISTICS:

151 (A) LENGTH: 8 amino acids

152 (B) TYPE: amino acid

153 (C) STRANDEDNESS: single

154 (D) TOPOLOGY: linear

## 156 (ii) MOLECULE TYPE: protein

## 158 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

160 Met Tyr Pro Glu Lys Lys Pro Val

161 1 5

## 164 (2) INFORMATION FOR SEQ ID NO: 7:

## 166 (i) SEQUENCE CHARACTERISTICS:

167 (A) LENGTH: 408 base pairs

168 (B) TYPE: nucleic acid

169 (C) STRANDEDNESS: single

170 (D) TOPOLOGY: linear

## 172 (ii) MOLECULE TYPE: DNA (genomic)

## 174 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

176 GAGCGAAGGA TACGGTCCAA GAGAAAAGAA ACCAGTGAGT ATTAATCACA ATATCGTAGA 60

178 GTACAATGAT GGTACTTTTA AATATCAATC TAGACCAAAA TTAACTCAA CACCTAAATA 120

180 TATTAAATTC AAACATGACT ATAATATTTT AGAATTTAAC GATGGTACAT TCGAATATGG 180

182 TGCACGTCCA CAATTTAATA AACCAGCAGC GAAACTGAT GCAACTATTA AAAAAGAACA 240

184 AAAATTGATT CAAGCTCAAA ATCTTGTGAG AGAATTTGAA AAAACACATA CTGTCAGTGC 300

186 ACACAGAAAA GCACAAAAGG CAGTCAACTT AGTTTCGTTT GAATACAAAG TGAAGAAAAT 360

188 GGTCTTACAA GAGCGAATTG ATAATGTATT AAAACAAGGA TTAGTGAG 408

## 191 (2) INFORMATION FOR SEQ ID NO: 8:

## 193 (i) SEQUENCE CHARACTERISTICS:

194 (A) LENGTH: 136 amino acids

195 (B) TYPE: amino acid

196 (C) STRANDEDNESS: single

197 (D) TOPOLOGY: linear

## 199 (ii) MOLECULE TYPE: protein

## 201 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

203 Ser Glu Gly Tyr Gly Pro Arg Glu Lys Lys Pro Val Ser Ile Asn His

204 1 5 10 15

206 Asn Ile Val Glu Tyr Asn Asp Gly Thr Phe Lys Tyr Gln Ser Arg Pro

207 20 25 30

209 Lys Phe Asn Ser Thr Pro Lys Tyr Ile Lys Phe Lys His Asp Tyr Asn

210 35 40 45

212 Ile Leu Glu Phe Asn Asp Gly Thr Phe Glu Tyr Gly Ala Arg Pro Gln

213 50 55 60

215 Phe Asn Lys Pro Ala Ala Lys Thr Asp Ala Thr Ile Lys Lys Glu Gln

216 65 70 75 80

218 Lys Leu Ile Gln Ala Gln Asn Leu Val Arg Glu Phe Glu Lys Thr His

219 85 90 95

221 Thr Val Ser Ala His Arg Lys Ala Gln Lys Ala Val Asn Leu Val Ser

222 100 105 110

224 Phe Glu Tyr Lys Val Lys Lys Met Val Leu Gln Glu Arg Ile Asp Asn

225 115 120 125

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Input Set : N:\Crif3\RULE60\09938497.txt

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227      Val Leu Lys Gln Gly Leu Val Arg
228          130                      135
231 (2) INFORMATION FOR SEQ ID NO: 9:
232      (i) SEQUENCE CHARACTERISTICS:
233          (A) LENGTH: 1009 base pairs
234          (B) TYPE: nucleic acid
235          (C) STRANDEDNESS: single
236          (D) TOPOLOGY: linear
237      (ii) MOLECULE TYPE: DNA (genomic)
238      (ix) FEATURE:
239          (A) NAME/KEY: CDS
240          (B) LOCATION: 157..654
241      (ix) FEATURE:
242          (A) NAME/KEY: CDS
243          (B) LOCATION: 804..1007
244      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:
252 GACTAGTGTA TAAGTGCTGA TGAGTCACAA GATAGATAAC TATATTTTGT CTATATTATA      60
254 AAGTGTTTAT AGTTAATTAA TAATTAGTTA ATTTCAAAAG TTGTATAAAT AGGATAACTT      120
256 AATAAATGTA AGATAATAAT TTGGAGGATA ATTAAC ATG AAA AAT AAA TTG ATA      174
257                               Met Lys Asn Lys Leu Ile
258                               1                      5
260 GCA AAA TCT TTA TTA ACA ATA GCG GCA ATT GGT ATT ACT ACA ACT ACA      222
261 Ala Lys Ser Leu Leu Thr Ile Ala Ala Ile Gly Ile Thr Thr Thr Thr
262          10                      15                      20
264 ATT GCG TCA ACA GCA GAT GCG AGC GAA GGA TAC GGT CCA AGA GAA AAG      270
265 Ile Ala Ser Thr Ala Asp Ala Ser Glu Gly Tyr Gly Pro Arg Glu Lys
266          25                      30                      35
268 AAA CCA GTG AGT ATT AAT CAC AAT ATC GTA GAG TAC AAT GAT GGT ACT      318
269 Lys Pro Val Ser Ile Asn His Asn Ile Val Glu Tyr Asn Asp Gly Thr
270          40                      45                      50
272 TTT AAA TAT CAA TCT AGA CCA AAA TTT AAC TCA ACA CCT AAA TAT ATT      366
273 Phe Lys Tyr Gln Ser Arg Pro Lys Phe Asn Ser Thr Pro Lys Tyr Ile
274          55                      60                      65                      70
276 AAA TTC AAA CAT GAC TAT AAT ATT TTA GAA TTT AAC GAT GGT ACA TTC      414
277 Lys Phe Lys His Asp Tyr Asn Ile Leu Glu Phe Asn Asp Gly Thr Phe
278          75                      80                      85
280 GAA TAT GGT GCA CGT CCA CAA TTT AAT AAA CCA GCA GCG AAA ACT GAT      462
281 Glu Tyr Gly Ala Arg Pro Gln Phe Asn Lys Pro Ala Ala Lys Thr Asp
282          90                      95                      100
284 GCA ACT ATT AAA AAA GAA CAA AAA TTG ATT CAA GCT CAA AAT CTT GTG      510
285 Ala Thr Ile Lys Lys Glu Gln Lys Leu Ile Gln Ala Gln Asn Leu Val
286          105                      110                      115
288 AGA GAA TTT GAA AAA ACA CAT ACT GTC AGT GCA CAC AGA AAA GCA CAA      558
289 Arg Glu Phe Glu Lys Thr His Thr Val Ser Ala His Arg Lys Ala Gln
290          120                      125                      130
292 AAG GCA GTC AAC TTA GTT TCG TTT GAA TAC AAA GTG AAG AAA ATG GTC      606
293 Lys Ala Val Asn Leu Val Ser Phe Glu Tyr Lys Val Lys Lys Met Val
294          135                      140                      145                      150
296 TTA CAA GAG CGA ATT GAT AAT GTA TTA AAA CAA GGA TTA GTG AGA TAA      654

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297 Leu Gln Glu Arg Ile Asp Asn Val Leu Lys Gln Gly Leu Val Arg  *
298              155              160              165
300 TACTTCTGTC ATTATTTTAA GTTCAAAATA ATTTAATATT ATATTATTTT TTATTAATAA 714
302 AACGACTATG CTATTTAATG CCAGGTTAAT GTAACTTTCC TAAAATTGAC TATATAATCG 774
304 TTAAGTATCA ATTTTAAGGA GAGTTTACA ATG AAA TTT AAA AAA TAT ATA TTA 827
305                               Met Lys Phe Lys Lys Tyr Ile Leu
W--> 306                               1           5
308 ACA GGA ACA TTA GCA TTA CTT TTA TCA TCA ACT GGG ATA GCA ACT ATA 875
309 Thr Gly Thr Leu Ala Leu Leu Leu Ser Ser Thr Gly Ile Ala Thr Ile
W--> 310      10              15              20
312 GAA GGG AAT AAA GCA GAT GCA AGT AGT CTG GAC AAA TAT TTA ACT GAA 923
313 Glu Gly Asn Lys Ala Asp Ala Ser Ser Leu Asp Lys Tyr Leu Thr Glu
W--> 314  25      30      35      40
316 AGT CAG TTT CAT GAT AAA CGC ATA GCA GAA GAA TTA AGA ACT TTA CTT 971
317 Ser Gln Phe His Asp Lys Arg Ile Ala Glu Leu Arg Thr Leu Leu
W--> 318              45              50              55
320 AAC AAA TCG AAT GTA TAT GCA TTA GCT GCA GGA AGC TT 1009
321 Asn Lys Ser Asn Val Tyr Ala Leu Ala Ala Gly Ser
W--> 322      60              65
325 (2) INFORMATION FOR SEQ ID NO: 10:
327   (i) SEQUENCE CHARACTERISTICS:
328       (A) LENGTH: 781 base pairs
329       (B) TYPE: nucleic acid
330       (C) STRANDEDNESS: single
331       (D) TOPOLOGY: linear
333   (ii) MOLECULE TYPE: DNA (genomic)
335   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:
337 ATAGATAACT ATATTTTGTC TATATTATAA AGTGTTTATA GTTAATTAAT AATTAGTTAA 60
339 TTTCAAAAGT TGTATAAATA GGATAACTTA ATAAATGTAA GATAATAATT TGGAGGATAA 120
341 TTAACATGAA AAATAAATTG ATAGCAAAAT CTTTATTAAC AATAGCGGCA ATTGGTATTA 180
343 CTACAACACT AATTGCGTCA ACAGCAGATG CGAGCGAAGG ATACGGTCCA AGAGAAAAGA 240
345 AACCAGTGAG TATTAATCAC AATATCGTAG AGTACAATGA TGGTACTTTT AAATATCAAT 300
347 CTAGACCAAA ATTTAACTCA ACACCTAAAT ATATTAATTT CAAACATGAC TATAATATTT 360
349 TAGAATTTAA CGATGGTACA TTCGAATATG GTGCACGTCC ACAATTTAAT AAACCAGCAG 420
351 CGAAAACACT TGCAACTATT AAAAAAGAAC AAAAATTGAT TCAAGCTCAA AATCTTGTGA 480
353 GAGAATTTGA AAAAACACAT ACTGTCAGTG CACACAGAAA AGCACAAAAG GCAGTCAACT 540
355 TAGTTTCGTT TGAATACAAA GTGAAGAAAA TGGTCTTACA AGAGCGAATT GATAATGTAT 600
357 TAAAACAAGG ATTAGTGAGA TAATACTTCT GTCATTATTT TAAGTTCAAA ATAATTTAAT 660
359 ATTATATTAT TTTTATTATA TAAAACGACT ATGCTATTTA ATGCCAGGTT AATGTAACCT 720
361 TCCTAAATTA GACTATATAA TCGTTAAGTA TCAATTTTAA GGAGAGTTTA CAATGAAATT 780
363 T 781
366 (2) INFORMATION FOR SEQ ID NO: 11:
368   (i) SEQUENCE CHARACTERISTICS:
369       (A) LENGTH: 785 base pairs
370       (B) TYPE: nucleic acid
371       (C) STRANDEDNESS: single
372       (D) TOPOLOGY: linear
374   (ii) MOLECULE TYPE: DNA (genomic)
376   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

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## VERIFICATION SUMMARY

PATENT APPLICATION: US/09/938,497

DATE: 10/31/2001

TIME: 12:04:26

Input Set : N:\Crif3\RULE60\09938497.txt

Output Set: N:\CRF3\10312001\I938497.raw

L:27 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]  
L:28 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]  
L:306 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9  
L:310 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9  
L:314 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9  
L:318 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9  
L:322 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9